

SEQUENCE LISTING

<110> Trotta, Christopher R.

<120> TARGETING ENZYMES OF THE tRNA SPLICING
PATHWAY FOR IDENTIFICATION OF ANTI-FUNGAL AND/OR
ANTI-PROLIFERATIVE MOLECULES

<130> 10589-034-999

<140> US/10/551,300

<141> 2005-09-27

<150> PCT/US2004/009590

<151> 2004-03-26

<150> 60/458,067

<151> 2003-03-27

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 465

<212> PRT

<213> Homo sapiens

<220>

<223> HsSen2p

<400> 1

Met	Ala	Glu	Ala	Val	Phe	His	Ala	Pro	Lys	Arg	Lys	Arg	Arg	Val	Tyr	1	5	10	15
Glu	Thr	Tyr	Glu	Ser	Pro	Leu	Pro	Ile	Pro	Phe	Gly	Gln	Asp	His	Gly	20	25	30	
Pro	Leu	Lys	Glu	Phe	Lys	Ile	Phe	Arg	Ala	Glu	Met	Ile	Asn	Asn	Asn	35	40	45	
Val	Ile	Val	Arg	Asn	Ala	Glu	Asp	Ile	Glu	Gln	Leu	Tyr	Gly	Lys	Gly	50	55	60	
Tyr	Phe	Gly	Lys	Gly	Ile	Leu	Ser	Arg	Ser	Arg	Pro	Ser	Phe	Thr	Ile	65	70	75	80
Ser	Asp	Pro	Lys	Leu	Val	Ala	Lys	Trp	Lys	Asp	Met	Lys	Thr	Asn	Met	85	90	95	
Pro	Ile	Ile	Thr	Ser	Lys	Arg	Tyr	Gln	His	Ser	Val	Glu	Trp	Ala	Ala	100	105	110	
Glu	Leu	Met	Arg	Arg	Gln	Gly	Gln	Asp	Glu	Ser	Thr	Val	Arg	Arg	Ile	115	120	125	
Leu	Lys	Asp	Tyr	Thr	Lys	Pro	Leu	Glu	His	Pro	Pro	Val	Lys	Arg	Asn	130	135	140	
Glu	Glu	Ala	Gln	Val	His	Asp	Lys	Leu	Asn	Ser	Gly	Met	Val	Ser	Asn	145	150	155	160
Met	Glu	Gly	Thr	Ala	Gly	Gly	Glu	Arg	Pro	Ser	Val	Val	Asn	Gly	Asp	165	170	175	
Ser	Gly	Lys	Ser	Gly	Gly	Val	Gly	Asp	Pro	Arg	Glu	Pro	Leu	Gly	Cys	180	185	190	
Leu	Gln	Glu	Gly	Ser	Gly	Cys	His	Pro	Thr	Thr	Glu	Ser	Phe	Glu	Lys	195	200	205	
Ser	Val	Arg	Glu	Asp	Ala	Ser	Pro	Leu	Pro	His	Val	Cys	Cys	Cys	Lys	210	215	220	

Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
 225 230 235 240
 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
 245 250 255
 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
 260 265 270
 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
 275 280 285
 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Ala
 290 295 300
 Phe Phe Leu Val Tyr Ala Leu Gly Cys Leu Ser Ile Tyr Tyr Glu Lys
 305 310 315 320
 Glu Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln
 325 330 335
 Pro Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys
 340 345 350
 Gly Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu
 355 360 365
 Tyr Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile
 370 375 380
 Glu Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser
 385 390 395 400
 Trp Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys
 405 410 415
 Glu Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys
 420 425 430
 Glu Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val
 435 440 445
 Ile Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp
 450 455 460
 Leu
 465

<210> 2
 <211> 448
 <212> PRT
 <213> Homo sapiens

<220>
 <223> HsSen2 variant

<400> 2
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 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
 20 25 30
 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
 35 40 45
 Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
 50 55 60
 Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
 65 70 75 80
 Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
 85 90 95
 Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
 100 105 110
 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
 115 120 125
 Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
 130 135 140

Glu	Glu	Ala	Gln	Val	His	Asp	Lys	Leu	Asn	Ser	Gly	Met	Val	Ser	Asn
145					150					155					160
Met	Glu	Gly	Thr	Ala	Gly	Gly	Glu	Arg	Pro	Ser	Val	Val	Asn	Gly	Asp
				165					170						175
Ser	Gly	Lys	Ser	Gly	Gly	Val	Gly	Asp	Pro	Arg	Glu	Pro	Leu	Gly	Cys
			180					185					190		
Leu	Gln	Glu	Gly	Ser	Gly	Cys	His	Pro	Thr	Thr	Glu	Ser	Phe	Glu	Lys
		195					200					205			
Ser	Val	Arg	Glu	Asp	Ala	Ser	Pro	Leu	Pro	His	Val	Cys	Cys	Cys	Lys
	210					215					220				
Gln	Asp	Ala	Leu	Ile	Leu	Gln	Arg	Gly	Leu	His	His	Glu	Asp	Gly	Ser
225					230					235					240
Gln	His	Ile	Gly	Leu	Leu	His	Pro	Gly	Asp	Arg	Gly	Pro	Asp	His	Glu
			245						250					255	
Tyr	Val	Leu	Val	Glu	Glu	Ala	Glu	Cys	Ala	Met	Ser	Glu	Arg	Glu	Ala
			260					265					270		
Ala	Pro	Asn	Glu	Glu	Leu	Val	Gln	Arg	Asn	Arg	Leu	Ile	Cys	Arg	Arg
		275					280					285			
Asn	Pro	Tyr	Arg	Ile	Phe	Glu	Tyr	Leu	Gln	Leu	Ser	Leu	Glu	Glu	Glu
	290					295					300				
Pro	Leu	Thr	Ile	Val	Lys	Leu	Trp	Lys	Ala	Phe	Thr	Val	Val	Gln	Pro
305					310					315					320
Thr	Phe	Arg	Thr	Thr	Tyr	Met	Ala	Tyr	His	Tyr	Phe	Arg	Ser	Lys	Gly
				325					330					335	
Trp	Val	Pro	Lys	Val	Gly	Leu	Lys	Tyr	Gly	Thr	Asp	Leu	Leu	Leu	Tyr
			340					345					350		
Arg	Lys	Gly	Pro	Pro	Phe	Tyr	His	Ala	Ser	Tyr	Ser	Val	Ile	Ile	Glu
		355					360					365			
Leu	Val	Asp	Asp	His	Phe	Glu	Gly	Ser	Leu	Arg	Arg	Pro	Leu	Ser	Trp
	370					375					380				
Lys	Ser	Leu	Ala	Ala	Leu	Ser	Arg	Val	Ser	Val	Asn	Val	Ser	Lys	Glu
385					390					395					400
Leu	Met	Leu	Cys	Tyr	Leu	Ile	Lys	Pro	Ser	Thr	Met	Thr	Asp	Lys	Glu
				405					410					415	
Met	Glu	Ser	Pro	Glu	Cys	Met	Lys	Arg	Ile	Lys	Val	Gln	Glu	Val	Ile
			420					425					430		
Leu	Ser	Arg	Trp	Val	Ser	Ser	Arg	Glu	Arg	Ser	Asp	Gln	Asp	Asp	Leu
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<210> 3
 <211> 377
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <223> Sc Sen2p

<400> 3
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 Ile His Pro Val Asp Asp Leu Pro Glu Leu Ile Leu His Asn Pro Leu
 20 25 30
 Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu
 35 40 45
 Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Thr Leu His Ile
 50 55 60
 Thr Val Gln Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe
 65 70 75 80
 Phe Gly Thr Gly Gln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg
 85 90 95

Thr	Glu	Ala	Arg	Leu	Gly	Leu	Asn	Asp	Thr	Pro	Leu	His	Asn	Arg	Gly	
			100					105					110			
Gly	Thr	Lys	Ser	Asn	Thr	Glu	Thr	Glu	Met	Thr	Leu	Glu	Lys	Val	Thr	
		115					120					125				
Gln	Gln	Arg	Arg	Leu	Gln	Arg	Leu	Glu	Phe	Lys	Lys	Glu	Arg	Ala	Lys	
		130				135					140					
Leu	Glu	Arg	Glu	Leu	Leu	Glu	Leu	Arg	Lys	Lys	Gly	Gly	His	Ile	Asp	
145					150					155					160	
Glu	Glu	Asn	Ile	Leu	Leu	Glu	Lys	Gln	Arg	Glu	Ser	Leu	Arg	Lys	Phe	
			165				170							175		
Lys	Leu	Lys	Gln	Thr	Glu	Asp	Val	Gly	Ile	Val	Ala	Gln	Gln	Gln	Asp	
			180					185					190			
Ile	Ser	Glu	Ser	Asn	Leu	Arg	Asp	Glu	Asp	Asn	Asn	Leu	Leu	Asp	Glu	
		195					200					205				
Asn	Gly	Asp	Leu	Leu	Pro	Leu	Glu	Ser	Leu	Glu	Leu	Met	Pro	Val	Glu	
		210				215					220					
Ala	Met	Phe	Leu	Thr	Phe	Ala	Leu	Pro	Val	Leu	Asp	Ile	Ser	Pro	Ala	
225					230					235					240	
Cys	Leu	Ala	Gly	Lys	Leu	Phe	Gln	Phe	Asp	Ala	Lys	Tyr	Lys	Asp	Ile	
			245					250						255		
His	Ser	Phe	Val	Arg	Ser	Tyr	Val	Ile	Tyr	His	His	Tyr	Arg	Ser	His	
			260					265					270			
Gly	Trp	Cys	Val	Arg	Ser	Gly	Ile	Lys	Phe	Gly	Cys	Asp	Tyr	Leu	Leu	
		275					280					285				
Tyr	Lys	Arg	Gly	Pro	Pro	Phe	Gln	His	Ala	Glu	Phe	Cys	Val	Met	Gly	
		290				295					300					
Leu	Asp	His	Asp	Val	Ser	Lys	Asp	Tyr	Thr	Trp	Tyr	Ser	Ser	Ile	Ala	
305					310					315					320	
Arg	Val	Val	Gly	Gly	Ala	Lys	Lys	Thr	Phe	Val	Leu	Cys	Tyr	Val	Glu	
			325					330						335		
Arg	Leu	Ile	Ser	Glu	Gln	Glu	Ala	Ile	Ala	Leu	Trp	Lys	Ser	Asn	Asn	
			340				345						350			
Phe	Thr	Lys	Leu	Phe	Asn	Ser	Phe	Gln	Val	Gly	Glu	Val	Leu	Tyr	Lys	
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Arg	Trp	Val	Pro	Gly	Arg	Asn	Arg	Asp								
		370				375										

<210> 4

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif of the active site for the 5' splice site of yeast and archael tRNA splicing endonuclease

<400> 4

Tyr Arg Gly Gly Tyr

1

5